

SequenceListing-73670826.txt
SEQUENCE LISTING

<110> BEBBINGTON, CHRISTOPHER ROBERT
YU, BO

<120> TRANSACTIVATION SYSTEM FOR MAMMALIAN CELLS

<130> 73678-026

<140> 10/585,149

<141> 2006-06-30

<150> PCT/US2004/043830

<151> 2004-12-30

<150> 60/533,917

<151> 2003-12-13

<160> 56

<170> PatentIn version 3.5

<210> 1

<211> 236

<212> PRT

<213> Cricetulus longicaudatus

<400> 1

Met Ala Gln Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
1 5 10 15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Val
20 25 30

Gly Asp Val Asp Ala Ala Pro Leu Gly Ala Ala Pro Thr Pro Gly Ile
35 40 45

Phe Ser Phe Gln Pro Glu Ser Asn Pro Thr Pro Ala Val His Arg Asp
50 55 60

Met Ala Ala Arg Thr Ser Pro Leu Arg Pro Ile Val Ala Thr Thr Gly
65 70 75 80

Pro Thr Leu Ser Pro Val Pro Pro Val Val His Leu Thr Leu Arg Arg
85 90 95

Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Arg Asp Phe Ala Glu Met
100 105 110

Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly Arg Phe Ala
115 120 125

Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile
130 135 140

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Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu Ser Val Asn
145 150 155 160

Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp Met Thr Glu
165 170 175

Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn Gly Gly Trp
180 185 190

Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Val Arg Pro Leu Phe Asp
195 200 205

Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala Leu Val Gly
210 215 220

Ala Cys Ile Thr Leu Gly Thr Tyr Leu Gly His Lys
225 230 235

<210> 2
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<212> PRT
<213> Cricetulus longicaudatus

<400> 2
Met Ala Gln Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
1 5 10 15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Val
20 25 30

Gly Asp Val Asp Ala Ala Ala Ala Ala Ser Pro Val Pro Pro Val
35 40 45

Val His Leu Thr Leu Arg Arg Ala Gly Asp Asp Phe Ser Arg Arg Tyr
50 55 60

Arg Arg Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe
65 70 75 80

Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp
85 90 95

Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val
100 105 110

Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn
115 120 125

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Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp
130 135 140

Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro
145 150 155 160

Ser Val Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu
165 170 175

Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Thr Tyr Leu
180 185 190

Gly His Lys
195

<210> 3
<211> 588
<212> DNA
<213> Cricetulus longicaudatus

<400> 3
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tataagctgt cacagagggg ctacgagtgg gatgtgggag atgtggacgc cgcggccgcg 120
gccgcgagcc ccgtgccacc tgtggtccac ctgaccctcc gccgggctgg ggatgacttc 180
tcccgtcgct accgtcgga cttcgcgag atgtccagtc agctgcacct gacgcccttc 240
accgcgaggg gacgctttgc tacggtggtg gaggaactct tcagggatgg ggtgaactgg 300
gggaggattg tggccttctt tgagtctggt ggggtcatgt gtgtggagag cgtcaacagg 360
gagatgtcac ccctggtgga caacatcgcc ctgtggatga ccgagtacct gaaccggcat 420
ctgcacacct ggatccagga taacggaggc tgggacgcat ttgtggaact gtacggcccc 480
agtgtgaggg ctctgtttga tttctcttgg ctgtctctga agaccctgct cagcctggcc 540
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<210> 4
<211> 289
<212> PRT
<213> Human adenovirus type 5

<400> 4
Met Arg His Ile Ile Cys His Gly Gly Val Ile Thr Glu Glu Met Ala
1 5 10 15

Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu Ala Asp Asn Leu
20 25 30

Pro Pro Pro Ser His Phe Glu Pro Pro Thr Leu His Glu Leu His Asp
35 40 45

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Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu Ala Val Ser Gln
 50 55 60
 Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu Gly Ile Asp Leu
 65 70 75 80
 Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro Pro His Leu Ser
 85 90 95
 Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly Pro Val Ser Met
 100 105 110
 Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Gly His Glu Ala Gly
 115 120 125
 Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Glu Glu Phe Val Leu
 130 135 140
 Asp Tyr Val Glu His Pro Gly His Gly Cys Arg Ser Cys His Tyr His
 145 150 155 160
 Arg Arg Asn Thr Gly Asp Pro Asp Ile Met Cys Ser Leu Cys Tyr Met
 165 170 175
 Arg Thr Cys Gly Met Phe Val Tyr Ser Pro Val Ser Glu Pro Glu Pro
 180 185 190
 Glu Pro Glu Pro Glu Pro Glu Pro Ala Arg Pro Thr Arg Arg Pro Lys
 195 200 205
 Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro Val Ser Arg Glu
 210 215 220
 Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro Ser Asn Thr Pro
 225 230 235 240
 Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile Lys Pro Val Ala
 245 250 255
 Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys Ile Glu Asp Leu
 260 265 270
 Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys Lys Arg Pro Arg
 275 280 285

Pro

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<210> 5
 <211> 986
 <212> DNA
 <213> Human adenovirus type 5

<400> 5
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 gaccagctga tcgaagaggt actggctgat aatcttccac ctctagcca ttttgaacca 120
 cctacccttc acgaactgca tgatttagac gtgacggccc ccgaagatcc caacgaggag 180
 gcggtttcgc agatttttcc cgactctgta atgttgccg tgaggaagg gattgactta 240
 ctcaattttc cgccggcgcc cggttctccg gagccgcctc acctttcccg gcagcccagag 300
 cagccggagc agagagcctt ggggtccggtt tctatgccaa accttggtacc ggaggtgatc 360
 gatcttaccg gccacgaggc tggctttcca ccagtgacg acgaggatga agagggtagag 420
 gagtttgtgt tagattatgt ggagcacccc gggcacggtt gcaggtcttg tcattatcac 480
 cggaggaata cgggggaccc agatattatg tgttcgcttt gctatatgag gacctgtggc 540
 atgtttgtct acagtaagtg aaaattatgg gcagtgggtg atagagtggg gggtttggtg 600
 tggttaatttt ttttttaatt ttacagttt tgtggtttta agaattttgt attgtgattt 660
 ttttaaaagg tcctgtgtct gaacctgagc ctgagcccga gccagaaccg gagcctgcaa 720
 gacctaccg ccgtcctaaa atggcgccctg ctatcctgag acgcccagaca tcacctgtgt 780
 ctagagaatg caatagtagt acggatagct gtgactccgg tccttctaac acacctcctg 840
 agatacaccg ggtggtcccg ctgtgcccc ttaaaccagt tgccgtgaga gttggtgggc 900
 gtcgccaggc tgtggaatgt atcgaggact tgcttaacga gcctgggcaa cctttggact 960
 tgagctgtaa acgccccagg ccataa 986

<210> 6
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 6
 cccgaattcg ccgccacat gagacatatt atctgccac 39

<210> 7
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 7
cccgtcgacc ttatggcctg gggcgttt 28

<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 8
cccgggtaccg ccgccaccat gagacatatt atctgccac 39

<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 9
cccgcggccg ccttatggcc tggggcgttt 30

<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 10
ggaggtgatc gatcttaccg gccac 25

<210> 11
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 11
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<210> 12
<211> 36
<212> DNA
<213> Artificial Sequence

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<220>
 <223> Description of Artificial Sequence: Synthetic primer
 <400> 12
 cgtcacgtct aaatcatgca gttcgtgaag ggtagg 36

<210> 13
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer
 <400> 13
 cccgaattcg ccgccacccat ggaggcttgg gagtgttt 38

<210> 14
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
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 <400> 14
 cccgtcgacc aacattcatt cccgaggggt 29

<210> 15
 <211> 558
 <212> DNA
 <213> Human adenovirus type 5

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 ttgctggaac agagctctaa cagtacctct tggttttgga ggtttctgtg gggctcatcc 120
 caggcaaagt tagtctgcag aattaaggag gattacaagt gggaatttga agagcttttg 180
 aaatcctgtg gtgagctgtt tgattctttg aatctgggtc accaggcgct tttccaagag 240
 aaggatcatca agactttgga tttttccaca ccggggcgcg ctgcggctgc tgttgctttt 300
 ttgagtttta taaaggataa atggagcgaa gaaacccatc tgagcggggg gtacctgctg 360
 gattttcttg ccatgcatct gtggagagcg gttgtgagac acaagaatcg cctgctactg 420
 ttgtcttccg tccgcccggc gataataccg acggaggagc agcagcagca gcaggaggaa 480
 gccaggcggc ggcggcagga gcagagccca tggaaccgga gagccggcct ggaccctcgg 540
 gaatgaatgt tggtcgac 558

<210> 16

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<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 16
cccgtcgacg ccgccacat gccgccc aaa accccccg 38

<210> 17
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 17
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<210> 18
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<212> DNA
<213> Homo sapiens

<220>
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Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr
1 5 10

gcc gcc gct gcc gcc gcg gaa ccc ccg gca ccg ccg ccg ccg ccc cct 99
Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro
15 20 25

cct gag gag gac cca gag cag gac agc ggc ccg gag gac ctg cct ctc 147
Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu
30 35 40

gtc agg ctt gag ttt gaa gaa aca gaa gaa cct gat ttt act gca tta 195
Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu
45 50 55 60

tgt cag aaa tta aag ata cca gat cat gtc aga gag aga gct tgg tta 243
Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu
65 70 75

act tgg gag aaa gtt tca tct gtg gat gga gta ttg gga ggt tat att 291
Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Tyr Ile
80 85 90

caa aag aaa aag gaa ctg tgg gga atc tgt atc ttt att gca cga gtt 339
Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Arg Val
95 100 105

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gac cta gat gag atg tcg ttc act tta ctg agc tac aga aaa aca tac Asp Leu Asp Glu Met Ser Phe Thr Leu Leu Ser Tyr Arg Lys Thr Tyr 110 115 120	387
gaa atc agt gtc cat aaa ttc ttt aac tta cta aaa gaa att gat acc Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr 125 130 135 140	435
agt acc aaa gtt gat aat gct atg tca aga ctg ttg aag aag tat gat Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp 145 150 155	483
gta ttg ttt gca ctc ttc agc aaa ttg gaa agg aca tgt gaa ctt ata Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile 160 165 170	531
tat ttg aca caa ccc agc agt tcg ata tct act gaa ata aat tct gca Tyr Leu Thr Gln Pro Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala 175 180 185	579
ttg gtg cta aaa gtt tct tgg atc aca ttt tta tta gct aaa ggg gaa Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu 190 195 200	627
gta tta caa atg gaa gat gat ctg gtg att tca ttt cag tta atg cta Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu 205 210 215 220	675
tgt gtc ctt gac tat ttt att aaa ctc tca cct ccc atg ttg ctc aaa Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys 225 230 235	723
gaa cca tat aaa aca gct gtt ata ccc att aat ggt tca cct cga aca Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr 240 245 250	771
ccc agg cga ggt cag aac agg agt gca cgg ata gca aaa caa cta gaa Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu 255 260 265	819
aat gat aca aga att att gaa gtt ctc tgt aaa gaa cat gaa tgt aat Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn 270 275 280	867
ata gat gag gtg aaa aat gtt tat ttc aaa aat ttt ata cct ttt atg Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met 285 290 295 300	915
aat tct ctt gga ctt gta aca tct aat gga ctt cca gag gtt gaa aat Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn 305 310 315	963
ctt tct aaa cga tac gaa gaa att tat ctt aaa aat aaa gat cta gat Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp 320 325 330	1011
cga aga tta ttt ttg gat cat gat aaa act ctt cag act gat tct ata Arg Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile 335 340 345	1059
gac agt ttt gaa aca cag aga aca cca cga aaa agt aac ctt gat gaa Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu 1107	1107

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350	355	360	
gag gtg aat ata att cct cca cac act cca gtt agg act gtt atg aac			1155
Glu Val Asn Ile Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn			
365	370	375	380
act atc caa caa tta atg atg att tta aat tct gca agt gat caa cct			1203
Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro			
	385	390	395
tca gaa aat ctg att tcc tat ttt aac aac tgc aca gtg aat cca aaa			1251
Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys			
	400	405	410
gaa agt ata ctg aaa aga gtg aag gat ata gga tac atc ttt aaa gag			1299
Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu			
	415	420	425
aaa ttt gct aaa gct gtg gga cag ggt tgt gtc gaa att gga tca cag			1347
Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln			
	430	435	440
cga tac aaa ctt gga gtt cgc ttg tat tac cga gta atg gaa tcc atg			1395
Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met			
	445	450	455
ctt aaa tca gaa gaa gaa cga tta tcc att caa aat ttt agc aaa ctt			1443
Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu			
	465	470	475
ctg aat gac aac att ttt cat atg tct tta ttg gcg tgc gct ctt gag			1491
Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu			
	480	485	490
gtt gta atg gcc aca tat agc aga agt aca tct cag aat ctt gat tct			1539
Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser			
	495	500	505
gga aca gat ttg tct ttc cca tgg att ctg aat gtg ctt aat tta aaa			1587
Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys			
	510	515	520
gcc ttt gat ttt tac aaa gtg atc gaa agt ttt atc aaa gca gaa ggc			1635
Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly			
	525	530	535
aac ttg aca aga gaa atg ata aaa cat tta gaa cga tgt gaa cat cga			1683
Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg			
	545	550	555
atc atg gaa tcc ctt gca tgg ctc tca gat tca cct tta ttt gat ctt			1731
Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu			
	560	565	570
att aaa caa tca aag gac cga gaa gga cca act gat cac ctt gaa tct			1779
Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser			
	575	580	585
gct tgt cct ctt aat ctt cct ctc cag aat aat cac act gca gca gat			1827
Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp			
	590	595	600
atg tat ctt tct cct gta aga tct cca aag aaa aaa ggt tca act acg			1875

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Met	Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Gly	Ser	Thr	Thr			
605					610					615				620			
cgt	gta	aat	tct	act	gca	aat	gca	gag	aca	caa	gca	acc	tca	gcc	ttc		1923
Arg	Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe		
				625					630					635			
cag	acc	cag	aag	cca	ttg	aaa	tct	acc	tct	ctt	tca	ctg	ttt	tat	aaa		1971
Gln	Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys		
			640					645					650				
aaa	gtg	tat	cgg	cta	gcc	tat	ctc	cgg	cta	aat	aca	ctt	tgt	gaa	cgc		2019
Lys	Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg		
		655					660					665					
ctt	ctg	tct	gag	cac	cca	gaa	tta	gaa	cat	atc	atc	tgg	acc	ctt	ttc		2067
Leu	Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe		
	670					675				680							
cag	cac	acc	ctg	cag	aat	gag	tat	gaa	ctc	atg	aga	gac	agg	cat	ttg		2115
Gln	His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu		
	685				690					695					700		
gac	caa	att	atg	atg	tgt	tcc	atg	tat	ggc	ata	tgc	aaa	gtg	aag	aat		2163
Asp	Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn		
				705					710					715			
ata	gac	ctt	aaa	ttc	aaa	atc	att	gta	aca	gca	tac	aag	gat	ctt	cct		2211
Ile	Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro		
			720					725					730				
cat	gct	gtt	cag	gag	aca	ttc	aaa	cgt	gtt	ttg	atc	aaa	gaa	gag	gag		2259
His	Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu		
		735					740					745					
tat	gat	tct	att	ata	gta	ttc	tat	aac	tcg	gtc	ttc	atg	cag	aga	ctg		2307
Tyr	Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu		
	750					755					760						
aaa	aca	aat	att	ttg	cag	tat	gct	tcc	acc	agg	ccc	cct	acc	ttg	tca		2355
Lys	Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser		
	765				770					775				780			
cca	ata	cct	cac	att	cct	cga	agc	cct	tac	aag	ttt	cct	agt	tca	ccc		2403
Pro	Ile	Pro	His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro		
				785					790				795				
tta	cgg	att	cct	gga	ggg	aac	atc	tat	att	tca	ccc	ctg	aag	agt	cca		2451
Leu	Arg	Ile	Pro	Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro		
			800					805					810				
tat	aaa	att	tca	gaa	ggt	ctg	cca	aca	cca	aca	aaa	atg	act	cca	aga		2499
Tyr	Lys	Ile	Ser	Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg		
		815					820					825					
tca	aga	atc	tta	gta	tca	att	ggt	gaa	tca	ttc	ggg	act	tct	gag	aag		2547
Ser	Arg	Ile	Leu	Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys		
	830					835					840						
ttc	cag	aaa	ata	aat	cag	atg	gta	tgt	aac	agc	gac	cgt	gtg	ctc	aaa		2595
Phe	Gln	Lys	Ile	Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys		
	845				850					855				860			

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aga agt gct gaa gga agc aac cct cct aaa cca ctg aaa aaa cta cgc	2643
Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg	
865 870 875	
ttt gat att gaa gga tca gat gaa gca gat gga agt aaa cat ctc cca	2691
Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro	
880 885 890	
gga gag tcc aaa ttt cag cag aaa ctg gca gaa atg act tct act cga	2739
Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg	
895 900 905	
aca cga atg caa aag cag aaa atg aat gat agc atg gat acc tca aac	2787
Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn	
910 915 920	
aag gaa gag aaa tgaggatctc aggaccggcg gccgc	2824
Lys Glu Glu Lys	
925	

<210> 19
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 <213> Homo sapiens

<400> 19
 Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala
 1 5 10 15

Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu Glu Asp
 20 25 30

Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu
 35 40 45

Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu
 50 55 60

Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
 65 70 75 80

Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys
 85 90 95

Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Arg Val Asp Leu Asp Glu
 100 105 110

Met Ser Phe Thr Leu Leu Ser Tyr Arg Lys Thr Tyr Glu Ile Ser Val
 115 120 125

His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val
 130 135 140

SequenceListing-73670826.txt

Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
 145 150 155 160
 Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln
 165 170 175
 Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
 180 185 190
 Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met
 195 200 205
 Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp
 210 215 220
 Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys
 225 230 235 240
 Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly
 245 250 255
 Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg
 260 265 270
 Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val
 275 280 285
 Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly
 290 295 300
 Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg
 305 310 315 320
 Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Arg Arg Leu Phe
 325 330 335
 Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu
 340 345 350
 Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Ile
 355 360 365
 Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln
 370 375 380
 Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu
 385 390 395 400

SequenceListing-73670826.txt

Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu
405 410 415

Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys
420 425 430

Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu
435 440 445

Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu
450 455 460

Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn
465 470 475 480

Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala
485 490 495

Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu
500 505 510

Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe
515 520 525

Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg
530 535 540

Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser
545 550 555 560

Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser
565 570 575

Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu
580 585 590

Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser
595 600 605

Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser
610 615 620

Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys
625 630 635 640

Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg
645 650 655

SequenceListing-73670826.txt

Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu
 660 665 670
 His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu
 675 680 685
 Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met
 690 695 700
 Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys
 705 710 715 720
 Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln
 725 730 735
 Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile
 740 745 750
 Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile
 755 760 765
 Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His
 770 775 780
 Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro
 785 790 795 800
 Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser
 805 810 815
 Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu
 820 825 830
 Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile
 835 840 845
 Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu
 850 855 860
 Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu
 865 870 875 880
 Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys
 885 890 895
 Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln

SequenceListing-73670826.txt

900

905

910

Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
 915 920 925

<210> 20
 <211> 1010
 <212> DNA
 <213> Rattus sp.

<220>
 <221> CDS
 <222> (16)..(996)

<400> 20
 gaattcgccg ccacc atg acc atg gac tct gga gca gac aac cag cag agt 51
 Met Thr Met Asp Ser Gly Ala Asp Asn Gln Gln Ser
 1 5 10

gga gat gca gct gta aca gaa gct gaa aac caa caa atg aca gtt caa 99
 Gly Asp Ala Ala Val Thr Glu Ala Glu Asn Gln Gln Met Thr Val Gln
 15 20 25

gcc cag cca cag att gcc aca tta gcc cag gta tct atg cca gca gct 147
 Ala Gln Pro Gln Ile Ala Thr Leu Ala Gln Val Ser Met Pro Ala Ala
 30 35 40

cat gca aca tca tct gct ccc acc gta act cta gta cag ctg ccc aat 195
 His Ala Thr Ser Ser Ala Pro Thr Val Thr Leu Val Gln Leu Pro Asn
 45 50 55 60

ggg cag aca gtt caa gtc cat gga gtc att cag gcg gcc cag cca tca 243
 Gly Gln Thr Val Gln Val His Gly Val Ile Gln Ala Ala Gln Pro Ser
 65 70 75

gtt att cag tct cca caa gtc caa aca gtt cag att tca act att gca 291
 Val Ile Gln Ser Pro Gln Val Gln Thr Val Gln Ile Ser Thr Ile Ala
 80 85 90

gaa agt gaa gat tca cag gag tca gtg gat agt gta act gat tcc caa 339
 Glu Ser Glu Asp Ser Gln Glu Ser Val Asp Ser Val Thr Asp Ser Gln
 95 100 105

aag cga agg gaa att ctt tca agg agg cct tcc ttc agg aaa att ttg 387
 Lys Arg Arg Glu Ile Leu Ser Arg Arg Pro Ser Phe Arg Lys Ile Leu
 110 115 120

aat gac tta tct tct gat gca cca gga gtg cca agg att gaa gaa gag 435
 Asn Asp Leu Ser Ser Asp Ala Pro Gly Val Pro Arg Ile Glu Glu Glu
 125 130 135 140

aag tct gaa gag gag gct tca gca cct gcc atc acc gct gta gcg gtg 483
 Lys Ser Glu Glu Glu Ala Ser Ala Pro Ala Ile Thr Ala Val Ala Val
 145 150 155

cca acg cca att tac cgg act agc agt gga cag tat att acc att acc 531
 Pro Thr Pro Ile Tyr Arg Thr Ser Ser Gly Gln Tyr Ile Thr Ile Thr
 160 165 170

cag aga gga gca ata cag ctg gct agc aat ggt acc gat ggg gta cag 579

SequenceListing-73670826.txt

Gln Arg Gly Ala Ile Gln Leu	Ala Ser Asn Gly Thr Asp Gly Val Gln	
175	180 185	
ggc ctg caa aca tta acc atg gcc aat gca gca gcc act cag ccg ggt		627
Gly Leu Gln Thr Leu Thr Met	Ala Asn Ala Ala Ala Thr Gln Pro Gly	
190	195 200	
act acc att cta cag tat gca cag acc act gat gga cag cag atc tta		675
Thr Thr Ile Leu Gln Tyr Ala Gln Thr Thr Asp Gly Gln Gln Ile Leu		
205	210 215 220	
gtg ccc agc aac caa gtt gtt gtt caa gct gcc tct gga gac gta caa		723
Val Pro Ser Asn Gln Val Val Val Gln Ala Ser Gly Asp Val Gln		
225	230 235	
aca tac cag att cgc aca gca ccc act agc act att gcc cct gga gtt		771
Thr Tyr Gln Ile Arg Thr Ala Pro Thr Ser Thr Ile Ala Pro Gly Val		
240	245 250	
gtt atg gca tcc tcc cca gca ctt cct aca cag cct gct gaa gaa gca		819
Val Met Ala Ser Ser Pro Ala Leu Pro Thr Gln Pro Ala Glu Glu Ala		
255	260 265	
gca cga aag aga gag gtc cgt cta atg aag aac agg gaa gca gct cgt		867
Ala Arg Lys Arg Glu Val Arg Leu Met Lys Asn Arg Glu Ala Ala Arg		
270	275 280	
gag tgt cgt aga aag aag aaa gaa tat gtg aaa tgt tta gaa aac aga		915
Glu Cys Arg Arg Lys Lys Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg		
285	290 295 300	
gtg gca gtg ctt gaa aat caa aac aag aca ttg att gag gag cta aaa		963
Val Ala Val Leu Glu Asn Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys		
305	310 315	
gca ctt aag gac ctt tac tgc cac aaa tca gat taatttggt cgac		1010
Ala Leu Lys Asp Leu Tyr Cys His Lys Ser Asp		
320	325	

<210> 21
 <211> 327
 <212> PRT
 <213> Rattus sp.

<400> 21
 Met Thr Met Asp Ser Gly Ala Asp Asn Gln Gln Ser Gly Asp Ala Ala
 1 5 10 15

Val Thr Glu Ala Glu Asn Gln Gln Met Thr Val Gln Ala Gln Pro Gln
 20 25 30

Ile Ala Thr Leu Ala Gln Val Ser Met Pro Ala Ala His Ala Thr Ser
 35 40 45

Ser Ala Pro Thr Val Thr Leu Val Gln Leu Pro Asn Gly Gln Thr Val
 50 55 60

Gln Val His Gly Val Ile Gln Ala Ala Gln Pro Ser Val Ile Gln Ser

SequenceListing-73670826.txt

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65              70              75              80
Pro Gln Val Gln Thr Val Gln Ile Ser Thr Ile Ala Glu Ser Glu Asp
      85              90              95
Ser Gln Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg Arg Glu
      100             105             110
Ile Leu Ser Arg Arg Pro Ser Phe Arg Lys Ile Leu Asn Asp Leu Ser
      115             120             125
Ser Asp Ala Pro Gly Val Pro Arg Ile Glu Glu Glu Lys Ser Glu Glu
      130             135             140
Glu Ala Ser Ala Pro Ala Ile Thr Ala Val Ala Val Pro Thr Pro Ile
      145             150             155             160
Tyr Arg Thr Ser Ser Gly Gln Tyr Ile Thr Ile Thr Gln Arg Gly Ala
      165             170             175
Ile Gln Leu Ala Ser Asn Gly Thr Asp Gly Val Gln Gly Leu Gln Thr
      180             185             190
Leu Thr Met Ala Asn Ala Ala Ala Thr Gln Pro Gly Thr Thr Ile Leu
      195             200             205
Gln Tyr Ala Gln Thr Thr Asp Gly Gln Gln Ile Leu Val Pro Ser Asn
      210             215             220
Gln Val Val Val Gln Ala Ala Ser Gly Asp Val Gln Thr Tyr Gln Ile
      225             230             235             240
Arg Thr Ala Pro Thr Ser Thr Ile Ala Pro Gly Val Val Met Ala Ser
      245             250             255
Ser Pro Ala Leu Pro Thr Gln Pro Ala Glu Glu Ala Ala Arg Lys Arg
      260             265             270
Glu Val Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu Cys Arg Arg
      275             280             285
Lys Lys Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val Ala Val Leu
      290             295             300
Glu Asn Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala Leu Lys Asp
      305             310             315             320

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Leu Tyr Cys His Lys Ser Asp
325

<210> 22
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 22
cccgaattcg ccgccaccat gaccatggac tctggagcag aca 43

<210> 23
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 23
gtcgcacccaa attaattctga tttgtggcag 30

<210> 24
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 24
gtcaagcaag cttgccgcca ccatgagaca tattatctgc cacgg 45

<210> 25
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 25
cgcagtctcg agttatggcc tggggcgttt acagctc 37

<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

SequenceListing-73670826.txt

primer

<400> 26
cacctaccct tcacgaactg catgatttag acgtgacggc c 41

<210> 27
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 27
ggccgtcacg tctaaatcat gcagttcgtg aagggtaggt g 41

<210> 28
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 28
cggagggtgat cgatcttacc ggccacgagg ctggctttcc ac 42

<210> 29
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 29
gtggaaagcc agcctcgtgg ccggtgaagat cgatcacctc cg 42

<210> 30
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 30
gtcaagcaag cttgccgcca ccatgaccat ggaatctgga gc 42

<210> 31
<211> 37
<212> DNA
<213> Artificial Sequence

SequenceListing-73670826.txt

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<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 31
cgcagtggat ccttaatctg atttgtggca gtaaagg          37

<210> 32
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 32
gtcattcaaa attttcctga aggaaggcct ccttgaaag          39

<210> 33
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 33
tctttcaagg aggccttcct tcaggaaaat tttgaatgac          40

<210> 34
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 34
ggcattccaa gcttactggt ggtaaagccg ccaccatgga ggcttgggag tgtttgg          57

<210> 35
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 35
gatcgactct agatcattcc cgaggggtcca ggccgg          36

<210> 36
<211> 38
<212> DNA

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 36

taaagccacc atggctcaag ctgggagAAC aggtatg

38

<210> 37

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 37

gatcgactct agatcacttg tggcccaggt aggtaccc

38

<210> 38

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 38

gtgggagatg tggacgccgc ggccgcggcc gcgagccccg tgccacctgt ggtcc

55

<210> 39

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 39

ggaccacagg tggcacgggg ctcgcggccg cggccgcggc gtccacatct cccac

55

<210> 40

<211> 891

<212> DNA

<213> Human adenovirus type 5

<220>

<221> CDS

<222> (16)..(882)

<400> 40

aagcttgccg ccacc atg aga cat att atc tgc cac gga ggt gtt att acc
Met Arg His Ile Ile Cys His Gly Gly Val Ile Thr
1 5 10

51

SequenceListing-73670826.txt

gaa gaa atg gcc gcc agt ctt ttg gac cag ctg atc gaa gag gta ctg Glu Glu Met Ala Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu 15 20 25	99
gct gat aat ctt cca cct cct agc cat ttt gaa cca cct acc ctt cac Ala Asp Asn Leu Pro Pro Ser His Phe Glu Pro Thr Leu His 30 35 40	147
gaa ctg tat gat tta gac gtg acg gcc ccc gaa gat ccc aac gag gag Glu Leu Tyr Asp Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu 45 50 55 60	195
gcg gtt tcg cag att ttt ccc gac tct gta atg ttg gcg gtg cag gaa Ala Val Ser Gln Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu 65 70 75	243
ggg att gac tta ctc act ttt ccg ccg gcg ccc ggt tct ccg gag ccg Gly Ile Asp Leu Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro 80 85 90	291
cct cac ctt tcc cgg cag ccc gag cag ccg gag cag aga gcc ttg ggt Pro His Leu Ser Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly 95 100 105	339
ccg gtt tct atg cca aac ctt gta ccg gag gtg atc gat ctt acc tgc Pro Val Ser Met Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Cys 110 115 120	387
cac gag gct ggc ttt cca ccc agt gac gac gag gat gaa gag ggt gag His Glu Ala Gly Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Glu 125 130 135 140	435
gag ttt gtg tta gat tat gtg gag cac ccc ggg cac ggt tgc agg tct Glu Phe Val Leu Asp Tyr Val Glu His Pro Gly His Gly Cys Arg Ser 145 150 155	483
tgt cat tat cac cgg agg aat acg ggg gac cca gat att atg tgt tcg Cys His Tyr His Arg Arg Asn Thr Gly Asp Pro Asp Ile Met Cys Ser 160 165 170	531
ctt tgc tat atg agg acc tgt ggc atg ttt gtc tac agt cct gtg tct Leu Cys Tyr Met Arg Thr Cys Gly Met Phe Val Tyr Ser Pro Val Ser 175 180 185	579
gaa cct gag cct gag ccc gag cca gaa ccg gag cct gca aga cct acc Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Ala Arg Pro Thr 190 195 200	627
cgc cgt cct aaa atg gcg cct gct atc ctg aga cgc ccg aca tca cct Arg Arg Pro Lys Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro 205 210 215 220	675
gtg tct aga gaa tgc aat agt agt acg gat agc tgt gac tcc ggt cct Val Ser Arg Glu Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro 225 230 235	723
tct aac aca cct cct gag ata cac ccg gtg gtc ccg ctg tgc ccc att Ser Asn Thr Pro Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile 240 245 250	771
aaa cca gtt gcc gtg aga gtt ggt ggg cgt cgc cag gct gtg gaa tgt Lys Pro Val Ala Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys 255 260 265 270	819

SequenceListing-73670826.txt

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255
260
265
atc gag gac ttg ctt aac gag cct ggg caa cct ttg gac ttg agc tgt      867
Ile Glu Asp Leu Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys
270                               275                               280

aaa cgc ccc agg cca taactcgag      891
Lys Arg Pro Arg Pro
285

<210> 41
<211> 891
<212> DNA
<213> Human adenovirus type 5

<220>
<221> CDS
<222> (16)..(882)

<400> 41
aagcttgccg ccacc atg aga cat att atc tgc cac gga ggt gtt att acc      51
          1      5      10
          Met Arg His Ile Ile Cys His Gly Gly Val Ile Thr

gaa gaa atg gcc gcc agt ctt ttg gac cag ctg atc gaa gag gta ctg      99
Glu Glu Met Ala Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu
15                               20                               25

gct gat aat ctt cca cct cct agc cat ttt gaa cca cct acc ctt cac      147
Ala Asp Asn Leu Pro Pro Pro Ser His Phe Glu Pro Pro Thr Leu His
30                               35                               40

gaa ctg cat gat tta gac gtg acg gcc ccc gaa gat ccc aac gag gag      195
Glu Leu His Asp Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu
45                               50                               55                               60

gcg gtt tcg cag att ttt ccc gac tct gta atg ttg gcg gtg cag gaa      243
Ala Val Ser Gln Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu
65                               70                               75

ggg att gac tta ctc act ttt ccg ccg gcg ccc ggt tct ccg gag ccg      291
Gly Ile Asp Leu Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro
80                               85                               90

cct cac ctt tcc cgg cag ccc gag cag ccg gag cag aga gcc ttg ggt      339
Pro His Leu Ser Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly
95                               100                               105

ccg gtt tct atg cca aac ctt gta ccg gag gtg atc gat ctt acc tgc      387
Pro Val Ser Met Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Cys
110                               115                               120

cac gag gct ggc ttt cca ccc agt gac gac gag gat gaa gag ggt gag      435
His Glu Ala Gly Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Glu
125                               130                               135                               140

gag ttt gtg tta gat tat gtg gag cac ccc ggg cac ggt tgc agg tct      483
Glu Phe Val Leu Asp Tyr Val Glu His Pro Gly His Gly Cys Arg Ser
145                               150                               155

tgt cat tat cac cgg agg aat acg ggg gac cca gat att atg tgt tcg      531

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SequenceListing-73670826.txt

Cys	His	Tyr	His	Arg	Arg	Asn	Thr	Gly	Asp	Pro	Asp	Ile	Met	Cys	Ser		
			160					165					170				
ctt	tgc	tat	atg	agg	acc	tgt	ggc	atg	ttt	gtc	tac	agt	cct	gtg	tct	579	
Leu	Cys	Tyr	Met	Arg	Thr	Cys	Gly	Met	Phe	Val	Tyr	Ser	Pro	Val	Ser		
		175					180					185					
gaa	cct	gag	cct	gag	ccc	gag	cca	gaa	ccg	gag	cct	gca	aga	cct	acc	627	
Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Ala	Arg	Pro	Thr		
	190					195					200						
cgc	cgt	cct	aaa	atg	gcg	cct	gct	atc	ctg	aga	cgc	ccg	aca	tca	cct	675	
Arg	Arg	Pro	Lys	Met	Ala	Pro	Ala	Ile	Leu	Arg	Arg	Pro	Thr	Ser	Pro		
205					210				215						220		
gtg	tct	aga	gaa	tgc	aat	agt	agt	acg	gat	agc	tgt	gac	tcc	ggg	cct	723	
Val	Ser	Arg	Glu	Cys	Asn	Ser	Ser	Thr	Asp	Ser	Cys	Asp	Ser	Gly	Pro		
				225					230					235			
tct	aac	aca	cct	cct	gag	ata	cac	ccg	gtg	gtc	ccg	ctg	tgc	ccc	att	771	
Ser	Asn	Thr	Pro	Pro	Glu	Ile	His	Pro	Val	Val	Pro	Leu	Cys	Pro	Ile		
			240					245					250				
aaa	cca	gtt	gcc	gtg	aga	gtt	ggg	ggg	cgt	cgc	cag	gct	gtg	gaa	tgt	819	
Lys	Pro	Val	Ala	Val	Arg	Val	Gly	Gly	Arg	Arg	Gln	Ala	Val	Glu	Cys		
		255					260					265					
atc	gag	gac	ttg	ctt	aac	gag	cct	ggg	caa	cct	ttg	gac	ttg	agc	tgt	867	
Ile	Glu	Asp	Leu	Leu	Asn	Glu	Pro	Gly	Gln	Pro	Leu	Asp	Leu	Ser	Cys		
	270					275					280						
aaa	cgc	ccc	agg	cca	taactcgag											891	
Lys	Arg	Pro	Arg	Pro													
285																	

<210> 42
 <211> 1047
 <212> DNA
 <213> Cricetulus longicaudatus

<220>
 <221> CDS
 <222> (16)..(1038)

<400>	42																
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		Met	Thr	Met	Glu	Ser	Gly	Ala	Asp	Asn	Gln	Gln	Ser				
		1				5					10						
gga	gat	gct	gct	gta	aca	gaa	gct	gaa	aat	caa	caa	atg	aca	gct	caa	99	
Gly	Asp	Ala	Ala	Val	Thr	Glu	Ala	Glu	Asn	Gln	Gln	Met	Thr	Ala	Gln		
		15				20						25					
gcc	caa	cca	cag	att	gcc	aca	tta	gcc	cag	gta	tcc	atg	cca	gca	gct	147	
Ala	Gln	Pro	Gln	Ile	Ala	Thr	Leu	Ala	Gln	Val	Ser	Met	Pro	Ala	Ala		
		30				35					40						
cat	gcg	aca	tca	tct	gct	ccc	act	gta	acc	tta	gtg	cag	ctg	ccc	aat	195	
His	Ala	Thr	Ser	Ser	Ala	Pro	Thr	Val	Thr	Leu	Val	Gln	Leu	Pro	Asn		
45					50					55					60		

SequenceListing-73670826.txt

ggg cag aca gtc caa gtc cat gga gtt att cag gcg gcc cag cca tca Gly Gln Thr Val Gln Val His Gly Val Ile Gln Ala Ala Gln Pro Ser 65 70 75	243
gtt att cag tct cca caa gtc caa aca gtt cag tct tcc tgt aag gac Val Ile Gln Ser Pro Gln Val Gln Thr Val Gln Ser Ser Cys Lys Asp 80 85 90	291
tta aaa aga ctt ttc tcc gga act cag att tca act att gca gaa agt Leu Lys Arg Leu Phe Ser Gly Thr Gln Ile Ser Thr Ile Ala Glu Ser 95 100 105	339
gag gat tca cag gaa tct gtg gat agt gta act gat tcc caa aag cga Glu Asp Ser Gln Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg 110 115 120	387
agg gaa att ctt tca agg agg cct tcc tac agg aaa att ttg aat gac Arg Glu Ile Leu Ser Arg Arg Pro Ser Tyr Arg Lys Ile Leu Asn Asp 125 130 135 140	435
tta tct tct gat gca cca ggg gtg cca agg att gaa gaa gaa aag tcg Leu Ser Ser Asp Ala Pro Gly Val Pro Arg Ile Glu Glu Glu Lys Ser 145 150 155	483
gaa gag gag act tca gcc cct gcc atc acc act gtg aca gtg cca act Glu Glu Glu Thr Ser Ala Pro Ala Ile Thr Thr Val Thr Val Pro Thr 160 165 170	531
ccg att tac cag aca agc agt ggg cag tat att gcc att acc cag gga Pro Ile Tyr Gln Thr Ser Ser Gly Gln Tyr Ile Ala Ile Thr Gln Gly 175 180 185	579
gga gct ata cag ctg gct aac aat ggt acc gat ggg gta cag ggc ctt Gly Ala Ile Gln Leu Ala Asn Asn Gly Thr Asp Gly Val Gln Gly Leu 190 195 200	627
cag aca tta acc atg acc aat gca gct gcc act cag ccg ggt acc act Gln Thr Leu Thr Met Thr Asn Ala Ala Ala Thr Gln Pro Gly Thr Thr 205 210 215 220	675
att cta cag tat gca cag acc act gat gga cag cag att cta gtg ccc Ile Leu Gln Tyr Ala Gln Thr Thr Asp Gly Gln Gln Ile Leu Val Pro 225 230 235	723
agc aac caa gtt gtt gtt caa gct gcc tct ggc gat gta caa aca tac Ser Asn Gln Val Val Val Gln Ala Ala Ser Gly Asp Val Gln Thr Tyr 240 245 250	771
caa att cgt aca gca ccc act agc acc atc gcc cct gga gtt gtt atg Gln Ile Arg Thr Ala Pro Thr Ser Thr Ile Ala Pro Gly Val Val Met 255 260 265	819
gca tcc tcc cca gca ctt cct acg cag cct gct gaa gaa gca gcc cgg Ala Ser Ser Pro Ala Leu Pro Thr Gln Pro Ala Glu Glu Ala Ala Arg 270 275 280	867
aag aga gag gtt cgt cta atg aag aac agg gaa gca gca aga gaa tgt Lys Arg Glu Val Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu Cys 285 290 295 300	915
cgt aga aag aag aaa gaa tat gtg aaa tgt tta gag aac aga gtg gca Arg Arg Lys Lys Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val Ala 305 310 315	963

SequenceListing-73670826.txt

gtg ctt gaa aac caa aac aag aca ttg att gag gag cta aaa gca ctt 1011
Val Leu Glu Asn Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala Leu
320 325 330

aag gac ctt tac tgc cac aaa tca gat taaggatcc 1047
Lys Asp Leu Tyr Cys His Lys Ser Asp
335 340

<210> 43

<211> 1047

<212> DNA

<213> Cricetulus longicaudatus

<220>

<221> CDS

<222> (16)..(1038)

<400> 43

aagcttgccg ccacc atg acc atg gaa tct gga gca gac aac cag cag agt 51
Met Thr Met Glu Ser Gly Ala Asp Asn Gln Gln Ser
1 5 10

gga gat gct gct gta aca gaa gct gaa aat caa caa atg aca gct caa 99
Gly Asp Ala Ala Val Thr Glu Ala Glu Asn Gln Gln Met Thr Ala Gln
15 20 25

gcc caa cca cag att gcc aca tta gcc cag gta tcc atg cca gca gct 147
Ala Gln Pro Gln Ile Ala Thr Leu Ala Gln Val Ser Met Pro Ala Ala
30 35 40

cat gcg aca tca tct gct ccc act gta acc tta gtg cag ctg ccc aat 195
His Ala Thr Ser Ser Ala Pro Thr Val Thr Leu Val Gln Leu Pro Asn
45 50 55 60

ggg cag aca gtc caa gtc cat gga gtt att cag gcg gcc cag cca tca 243
Gly Gln Thr Val Gln Val His Gly Val Ile Gln Ala Ala Gln Pro Ser
65 70 75

gtt att cag tct cca caa gtc caa aca gtt cag tct tcc tgt aag gac 291
Val Ile Gln Ser Pro Gln Val Gln Thr Val Gln Ser Ser Cys Lys Asp
80 85 90

tta aaa aga ctt ttc tcc gga act cag att tca act att gca gaa agt 339
Leu Lys Arg Leu Phe Ser Gly Thr Gln Ile Ser Thr Ile Ala Glu Ser
95 100 105

gag gat tca cag gaa tct gtg gat agt gta act gat tcc caa aag cga 387
Glu Asp Ser Gln Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg
110 115 120

agg gaa att ctt tca agg agg cct tcc tcc agg aaa att ttg aat gac 435
Arg Glu Ile Leu Ser Arg Arg Pro Ser Ser Arg Lys Ile Leu Asn Asp
125 130 135 140

tta tct tct gat gca cca ggg gtg cca agg att gaa gaa gaa aag tcg 483
Leu Ser Ser Asp Ala Pro Gly Val Pro Arg Ile Glu Glu Glu Lys Ser
145 150 155

gaa gag gag act tca gcc cct gcc atc acc act gtg aca gtg cca act 531
Glu Glu Glu Thr Ser Ala Pro Ala Ile Thr Thr Val Thr Val Pro Thr

SequenceListing-73670826.txt

160	165	170	
ccg att tac cag aca agc agt ggg cag tat att gcc att acc cag gga Pro Ile Tyr Gln Thr Ser Ser Gly Gln Tyr Ile Ala Ile Thr Gln Gly	175	180	185
gga gct ata cag ctg gct aac aat ggt acc gat ggg gta cag ggc ctt Gly Ala Ile Gln Leu Ala Asn Asn Gly Thr Asp Gly Val Gln Gly Leu	190	195	200
cag aca tta acc atg acc aat gca gct gcc act cag ccg ggt acc act Gln Thr Leu Thr Met Thr Asn Ala Ala Thr Gln Pro Gly Thr Thr	205	210	215
att cta cag tat gca cag acc act gat gga cag cag att cta gtg ccc Ile Leu Gln Tyr Ala Gln Thr Thr Asp Gly Gln Gln Ile Leu Val Pro	225	230	235
agc aac caa gtt gtt gtt caa gct gcc tct ggc gat gta caa aca tac Ser Asn Gln Val Val Val Gln Ala Ala Ser Gly Asp Val Gln Thr Tyr	240	245	250
caa att cgt aca gca ccc act agc acc atc gcc cct gga gtt gtt atg Gln Ile Arg Thr Ala Pro Thr Ser Thr Ile Ala Pro Gly Val Val Met	255	260	265
gca tcc tcc cca gca ctt cct acg cag cct gct gaa gaa gca gcc cgg Ala Ser Ser Pro Ala Leu Pro Thr Gln Pro Ala Glu Glu Ala Ala Arg	270	275	280
aag aga gag gtt cgt cta atg aag aac agg gaa gca gca aga gaa tgt Lys Arg Glu Val Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu Cys	285	290	295
cgt aga aag aag aaa gaa tat gtg aaa tgt tta gag aac aga gtg gca Arg Arg Lys Lys Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val Ala	305	310	315
gtg ctt gaa aac caa aac aag aca ttg att gag gag cta aaa gca ctt Val Leu Glu Asn Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala Leu	320	325	330
aag gac ctt tac tgc cac aaa tca gat taaggatcc Lys Asp Leu Tyr Cys His Lys Ser Asp	335	340	

<210> 44

<211> 564

<212> DNA

<213> Human adenovirus type 5

<220>

<221> CDS

<222> (28)..(555)

<400> 44

aagcttactg ttggtaaagc cgccacc atg gag gct tgg gag tgt ttg gaa gat	54
Met Glu Ala Trp Glu Cys Leu Glu Asp	
1 5	

ttt tct gct gtg cgt aac ttg ctg gaa cag agc tct aac agt acc tct	102
-----------------------------------------------------------------	-----

SequenceListing-73670826.txt

Phe	Ser	Ala	Val	Arg	Asn	Leu	Leu	Glu	Gln	Ser	Ser	Asn	Ser	Thr	Ser		
10					15					20					25		
tg	g	t	t	g	g	a	a	t	t	c	t	g	t	g	g	c	t
Trp	Phe	Trp	Arg	Phe	Leu	Trp	Gly	Ser	Ser	Gln	Ala	Lys	Leu	Val	Cys		150
				30					35				40				
aga	att	aag	gag	gat	tac	aag	tgg	gaa	ttt	gaa	gag	ctt	ttg	aaa	tcc		198
Arg	Ile	Lys	Glu	Asp	Tyr	Lys	Trp	Glu	Phe	Glu	Glu	Leu	Leu	Lys	Ser		
			45					50				55					
tgt	ggt	gag	ctg	ttt	gat	tct	ttg	aat	ctg	ggt	cac	cag	gcg	ctt	ttc		246
Cys	Gly	Glu	Leu	Phe	Asp	Ser	Leu	Asn	Leu	Gly	His	Gln	Ala	Leu	Phe		
		60					65					70					
caa	gag	aag	gtc	atc	aag	act	ttg	gat	ttt	tcc	aca	ccg	ggg	cg	gct		294
Gln	Glu	Lys	Val	Ile	Lys	Thr	Leu	Asp	Phe	Ser	Thr	Pro	Gly	Arg	Ala		
	75					80					85						
gcg	gct	gct	gtt	gct	ttt	ttg	agt	ttt	ata	aag	gat	aaa	tgg	agc	gaa		342
Ala	Ala	Ala	Val	Ala	Phe	Leu	Ser	Phe	Ile	Lys	Asp	Lys	Trp	Ser	Glu		
90					95					100					105		
gaa	acc	cat	ctg	agc	ggg	ggg	tac	ctg	ctg	gat	ttt	ctg	gcc	atg	cat		390
Glu	Thr	His	Leu	Ser	Gly	Gly	Tyr	Leu	Leu	Asp	Phe	Leu	Ala	Met	His		
				110					115					120			
ctg	tgg	aga	gcg	gtt	gtg	aga	cac	aag	aat	cgc	ctg	cta	ctg	ttg	tct		438
Leu	Trp	Arg	Ala	Val	Val	Arg	His	Lys	Asn	Arg	Leu	Leu	Leu	Leu	Ser		
			125					130					135				
tcc	gtc	cgc	ccg	gcg	ata	ata	ccg	acg	gag	gag	cag	cag	cag	cag	cag		486
Ser	Val	Arg	Pro	Ala	Ile	Ile	Pro	Thr	Glu	Glu	Gln	Gln	Gln	Gln	Gln		
		140					145					150					
gag	gaa	gcc	agg	cgg	cgg	cgg	cag	gag	cag	agc	cca	tgg	aac	ccg	aga		534
Glu	Glu	Ala	Arg	Arg	Arg	Arg	Gln	Glu	Gln	Ser	Pro	Trp	Asn	Pro	Arg		
	155					160					165						
gcc	ggc	ctg	gac	cct	cgg	gaa	tgatctaga										564
Ala	Gly	Leu	Asp	Pro	Arg	Glu											
170					175												

<210> 45
 <211> 596
 <212> DNA
 <213> Cricetulus longicaudatus

<220>
 <221> CDS
 <222> (3)..(587)

<400>	45																
cc	atg	gct	caa	gct	ggg	aga	aca	ggg	tat	gat	aac	cga	gag	atc	gtg		47
	Met	Ala	Gln	Ala	Gly	Arg	Thr	Gly	Tyr	Asp	Asn	Arg	Glu	Ile	Val		
	1				5				10					15			
atg	aag	tac	atc	cat	tat	aag	ctg	tca	cag	agg	ggc	tac	gag	tgg	gat		95
Met	Lys	Tyr	Ile	His	Tyr	Lys	Leu	Ser	Gln	Arg	Gly	Tyr	Glu	Trp	Asp		
				20					25					30			

SequenceListing-73670826.txt

gtg gga gat gtg gac gcc gcg gcc gcg gcc gcg agc ccc gtg cca cct Val Gly Asp Val Asp Ala Ala Ala Ala Ala Ser Pro Val Pro Pro	143
gtg gtc cac ctg acc ctc cgc cgg gct ggg gat gac ttc tcc cgt cgc Val Val His Leu Thr Leu Arg Arg Ala Gly Asp Asp Phe Ser Arg Arg	191
tac cgt cgc gac ttc gcg gag atg tcc agt cag ctg cac ctg acg ccc Tyr Arg Arg Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro	239
ttc acc gcg agg gga cgc ttt gct acg gtg gtg gag gaa ctc ttc agg Phe Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg	287
gat ggg gtg aac tgg ggg agg att gtg gcc ttc ttt gag ttc ggt ggg Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly	335
gtc atg tgt gtg gag agc gtc aac agg gag atg tca ccc ctg gtg gac Val Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp	383
aac atc gcc ctg tgg atg acc gag tac ctg aac cgg cat ctg cac acc Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr	431
tgg atc cag gat aac gga ggc tgg gac gca ttt gtg gaa ctg tac ggc Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly	479
ccc agt gtg agg cct ctg ttt gat ttc tct tgg ctg tct ctg aag acc Pro Ser Val Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr	527
ctg ctc agc ctg gcc ctg gtc ggg gcc tgc atc act ctg ggt acc tac Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Thr Tyr	575
ctg ggc cac aag tgatctaga Leu Gly His Lys	596

<210> 46

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 46

cgcagtacta gtttatggcc tggggcggtt acagctc

37

<210> 47

<211> 20

<212> DNA

<213> Artificial Sequence

SequenceListing-73670826.txt

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 47

gagctattcc agaagtagtg

20

<210> 48

<211> 289

<212> PRT

<213> Human adenovirus type 5

<400> 48

Met Arg His Ile Ile Cys His Gly Gly Val Ile Thr Glu Glu Met Ala
1 5 10 15

Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu Ala Asp Asn Leu
20 25 30

Pro Pro Pro Ser His Phe Glu Pro Pro Thr Leu His Glu Leu Tyr Asp
35 40 45

Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu Ala Val Ser Gln
50 55 60

Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu Gly Ile Asp Leu
65 70 75 80

Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro Pro His Leu Ser
85 90 95

Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly Pro Val Ser Met
100 105 110

Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Cys His Glu Ala Gly
115 120 125

Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Glu Glu Phe Val Leu
130 135 140

Asp Tyr Val Glu His Pro Gly His Gly Cys Arg Ser Cys His Tyr His
145 150 155 160

Arg Arg Asn Thr Gly Asp Pro Asp Ile Met Cys Ser Leu Cys Tyr Met
165 170 175

Arg Thr Cys Gly Met Phe Val Tyr Ser Pro Val Ser Glu Pro Glu Pro
180 185 190

SequenceListing-73670826.txt

Glu Pro Glu Pro Glu Pro Glu Pro Ala Arg Pro Thr Arg Arg Pro Lys
195 200 205

Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro Val Ser Arg Glu
210 215 220

Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro Ser Asn Thr Pro
225 230 235 240

Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile Lys Pro Val Ala
245 250 255

Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys Ile Glu Asp Leu
260 265 270

Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys Lys Arg Pro Arg
275 280 285

Pro

<210> 49
<211> 289
<212> PRT
<213> Human adenovirus type 5

<400> 49
Met Arg His Ile Ile Cys His Gly Gly Val Ile Thr Glu Glu Met Ala
1 5 10 15

Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu Ala Asp Asn Leu
20 25 30

Pro Pro Pro Ser His Phe Glu Pro Pro Thr Leu His Glu Leu His Asp
35 40 45

Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu Ala Val Ser Gln
50 55 60

Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu Gly Ile Asp Leu
65 70 75 80

Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro Pro His Leu Ser
85 90 95

Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly Pro Val Ser Met
100 105 110

Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Cys His Glu Ala Gly

115

120

125

Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Glu Glu Phe Val Leu
 130 135 140

Asp Tyr Val Glu His Pro Gly His Gly Cys Arg Ser Cys His Tyr His
 145 150 155 160

Arg Arg Asn Thr Gly Asp Pro Asp Ile Met Cys Ser Leu Cys Tyr Met
 165 170 175

Arg Thr Cys Gly Met Phe Val Tyr Ser Pro Val Ser Glu Pro Glu Pro
 180 185 190

Glu Pro Glu Pro Glu Pro Glu Pro Ala Arg Pro Thr Arg Arg Pro Lys
 195 200 205

Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro Val Ser Arg Glu
 210 215 220

Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro Ser Asn Thr Pro
 225 230 235 240

Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile Lys Pro Val Ala
 245 250 255

Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys Ile Glu Asp Leu
 260 265 270

Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys Lys Arg Pro Arg
 275 280 285

Pro

<210> 50

<211> 341

<212> PRT

<213> Cricetulus longicaudatus

<400> 50

Met Thr Met Glu Ser Gly Ala Asp Asn Gln Gln Ser Gly Asp Ala Ala
 1 5 10 15

Val Thr Glu Ala Glu Asn Gln Gln Met Thr Ala Gln Ala Gln Pro Gln
 20 25 30

Ile Ala Thr Leu Ala Gln Val Ser Met Pro Ala Ala His Ala Thr Ser
 35 40 45

SequenceListing-73670826.txt

Ser Ala Pro Thr Val Thr Leu Val Gln Leu Pro Asn Gly Gln Thr Val
50 55 60

Gln Val His Gly Val Ile Gln Ala Ala Gln Pro Ser Val Ile Gln Ser
65 70 75 80

Pro Gln Val Gln Thr Val Gln Ser Ser Cys Lys Asp Leu Lys Arg Leu
85 90 95

Phe Ser Gly Thr Gln Ile Ser Thr Ile Ala Glu Ser Glu Asp Ser Gln
100 105 110

Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg Arg Glu Ile Leu
115 120 125

Ser Arg Arg Pro Ser Tyr Arg Lys Ile Leu Asn Asp Leu Ser Ser Asp
130 135 140

Ala Pro Gly Val Pro Arg Ile Glu Glu Glu Lys Ser Glu Glu Glu Thr
145 150 155 160

Ser Ala Pro Ala Ile Thr Thr Val Thr Val Pro Thr Pro Ile Tyr Gln
165 170 175

Thr Ser Ser Gly Gln Tyr Ile Ala Ile Thr Gln Gly Gly Ala Ile Gln
180 185 190

Leu Ala Asn Asn Gly Thr Asp Gly Val Gln Gly Leu Gln Thr Leu Thr
195 200 205

Met Thr Asn Ala Ala Ala Thr Gln Pro Gly Thr Thr Ile Leu Gln Tyr
210 215 220

Ala Gln Thr Thr Asp Gly Gln Gln Ile Leu Val Pro Ser Asn Gln Val
225 230 235 240

Val Val Gln Ala Ala Ser Gly Asp Val Gln Thr Tyr Gln Ile Arg Thr
245 250 255

Ala Pro Thr Ser Thr Ile Ala Pro Gly Val Val Met Ala Ser Ser Pro
260 265 270

Ala Leu Pro Thr Gln Pro Ala Glu Glu Ala Ala Arg Lys Arg Glu Val
275 280 285

Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu Cys Arg Arg Lys Lys

290

295

300

Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val Ala Val Leu Glu Asn
305 310 315 320

Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala Leu Lys Asp Leu Tyr
325 330 335

Cys His Lys Ser Asp
340

<210> 51

<211> 341

<212> PRT

<213> Cricetulus longicaudatus

<400> 51

Met Thr Met Glu Ser Gly Ala Asp Asn Gln Gln Ser Gly Asp Ala Ala
1 5 10 15

Val Thr Glu Ala Glu Asn Gln Gln Met Thr Ala Gln Ala Gln Pro Gln
20 25 30

Ile Ala Thr Leu Ala Gln Val Ser Met Pro Ala Ala His Ala Thr Ser
35 40 45

Ser Ala Pro Thr Val Thr Leu Val Gln Leu Pro Asn Gly Gln Thr Val
50 55 60

Gln Val His Gly Val Ile Gln Ala Ala Gln Pro Ser Val Ile Gln Ser
65 70 75 80

Pro Gln Val Gln Thr Val Gln Ser Ser Cys Lys Asp Leu Lys Arg Leu
85 90 95

Phe Ser Gly Thr Gln Ile Ser Thr Ile Ala Glu Ser Glu Asp Ser Gln
100 105 110

Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg Arg Glu Ile Leu
115 120 125

Ser Arg Arg Pro Ser Ser Arg Lys Ile Leu Asn Asp Leu Ser Ser Asp
130 135 140

Ala Pro Gly Val Pro Arg Ile Glu Glu Glu Lys Ser Glu Glu Glu Thr
145 150 155 160

Ser Ala Pro Ala Ile Thr Thr Val Thr Val Pro Thr Pro Ile Tyr Gln
165 170 175

SequenceListing-73670826.txt

Thr Ser Ser Gly Gln Tyr Ile Ala Ile Thr Gln Gly Gly Ala Ile Gln
180 185 190

Leu Ala Asn Asn Gly Thr Asp Gly Val Gln Gly Leu Gln Thr Leu Thr
195 200 205

Met Thr Asn Ala Ala Ala Thr Gln Pro Gly Thr Thr Ile Leu Gln Tyr
210 215 220

Ala Gln Thr Thr Asp Gly Gln Gln Ile Leu Val Pro Ser Asn Gln Val
225 230 235 240

Val Val Gln Ala Ala Ser Gly Asp Val Gln Thr Tyr Gln Ile Arg Thr
245 250 255

Ala Pro Thr Ser Thr Ile Ala Pro Gly Val Val Met Ala Ser Ser Pro
260 265 270

Ala Leu Pro Thr Gln Pro Ala Glu Glu Ala Ala Arg Lys Arg Glu Val
275 280 285

Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu Cys Arg Arg Lys Lys
290 295 300

Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val Ala Val Leu Glu Asn
305 310 315 320

Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala Leu Lys Asp Leu Tyr
325 330 335

Cys His Lys Ser Asp
340

<210> 52

<211> 176

<212> PRT

<213> Human adenovirus type 5

<400> 52

Met Glu Ala Trp Glu Cys Leu Glu Asp Phe Ser Ala Val Arg Asn Leu
1 5 10 15

Leu Glu Gln Ser Ser Asn Ser Thr Ser Trp Phe Trp Arg Phe Leu Trp
20 25 30

Gly Ser Ser Gln Ala Lys Leu Val Cys Arg Ile Lys Glu Asp Tyr Lys
35 40 45

SequenceListing-73670826.txt

Trp Glu Phe Glu Glu Leu Leu Lys Ser Cys Gly Glu Leu Phe Asp Ser
50 55 60

Leu Asn Leu Gly His Gln Ala Leu Phe Gln Glu Lys Val Ile Lys Thr
65 70 75 80

Leu Asp Phe Ser Thr Pro Gly Arg Ala Ala Ala Ala Val Ala Phe Leu
85 90 95

Ser Phe Ile Lys Asp Lys Trp Ser Glu Glu Thr His Leu Ser Gly Gly
100 105 110

Tyr Leu Leu Asp Phe Leu Ala Met His Leu Trp Arg Ala Val Val Arg
115 120 125

His Lys Asn Arg Leu Leu Leu Leu Ser Ser Val Arg Pro Ala Ile Ile
130 135 140

Pro Thr Glu Glu Gln Gln Gln Gln Gln Glu Glu Ala Arg Arg Arg Arg
145 150 155 160

Gln Glu Gln Ser Pro Trp Asn Pro Arg Ala Gly Leu Asp Pro Arg Glu
165 170 175

<210> 53
<211> 195
<212> PRT
<213> Cricetulus longicaudatus

<400> 53
Met Ala Gln Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
1 5 10 15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Val
20 25 30

Gly Asp Val Asp Ala Ala Ala Ala Ala Ala Ser Pro Val Pro Pro Val
35 40 45

Val His Leu Thr Leu Arg Arg Ala Gly Asp Asp Phe Ser Arg Arg Tyr
50 55 60

Arg Arg Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe
65 70 75 80

Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp
85 90 95

SequenceListing-73670826.txt

Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val
100 105 110

Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn
115 120 125

Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp
130 135 140

Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro
145 150 155 160

Ser Val Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu
165 170 175

Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Thr Tyr Leu
180 185 190

Gly His Lys
195

<210> 54
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 54
Arg Ser Val Leu Thr Arg
1 5

<210> 55
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 55
Gly Gly Gly Gly Ser
1 5

<210> 56
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

peptide

<400> 56

Met Ala Tyr Pro Asp Tyr Val Pro Asp Tyr Ala Val
1 ; 5 10